



SEQUENCE LISTING

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Nagashima, Makoto
Government of United States as represented by the Secretary of the
Department of Health and Human Services

<120> New Tumor Suppressor Gene P33ING2

<130> 015280-376100US

<140> US 09/513,365

<141> 2000-02-25

<150> US 60/121,891

<151> 1999-02-26

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 280

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p33ING2
polypeptide sequence

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Thr Gly Glu Arg Ser Arg Leu Leu Thr Cys Tyr Val Gln Asp Tyr Leu
20 25 30

Glu Cys Val Glu Ser Leu Pro His Asp Met Gln Arg Asn Val Ser Val
35 40 45

Leu Arg Glu Leu Asp Asn Lys Tyr Gln Glu Thr Leu Lys Glu Ile Asp
50 55 60

Asp Val Tyr Glu Lys Tyr Lys Lys Glu Asp Asp Leu Asn Gln Lys Lys
65 70 75 80

Arg Leu Gln Gln Leu Leu Gln Arg Ala Leu Ile Asn Ser Gln Glu Leu
85 90 95

Gly Asp Glu Lys Ile Gln Ile Val Thr Gln Met Leu Glu Leu Val Glu
100 105 110

Asn Arg Ala Arg Gln Met Glu Leu His Ser Gln Cys Phe Gln Asp Pro
115 120 125

Ala Glu Ser Glu Arg Ala Ser Asp Lys Ala Lys Met Asp Ser Ser Gln
130 135 140

Pro Glu Arg Ser Ser Arg Arg Pro Arg Arg Gln Arg Thr Ser Glu Ser
145 150 155 160

Arg Asp Leu Cys His Met Ala Asn Gly Ile Glu Asp Cys Asp Asp Gln
 165 170 175
 Pro Pro Lys Glu Lys Lys Ser Lys Ser Ala Lys Lys Lys Lys Arg Ser
 180 185 190
 Lys Ala Lys Gln Glu Arg Glu Ala Ser Pro Val Glu Phe Ala Ile Asp
 195 200 205
 Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu
 210 215 220
 Met Ile Gly Cys Asp Asn Glu Gln Cys Pro Ile Glu Trp Phe His Phe
 225 230 235 240
 Ser Cys Val Ser Leu Thr Tyr Lys Pro Lys Gly Lys Trp Tyr Cys Pro
 245 250 255
 Lys Cys Arg Gly Asp Asn Glu Lys Thr Met Asp Lys Ser Thr Glu Lys
 260 265 270
 Thr Lys Lys Asp Arg Arg Ser Arg
 275 280

<210> 2
 <211> 1080
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: p33ING2
 nucleic acid sequence (GenBank Accession No.
 AF05053537)

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 ggagcggagc cggctgctca cctgctacgt gcaggactac cttgagtgcg tggagtgcgt 180
 gcccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaaga 240
 aacgttaaag gaaattgatg atgtctacga aaaatataag aaagaagatg atttaaacca 300
 gaagaaacgt ctacagcagc ttctccagag agcactaatt aatagtcaag aattgggaga 360
 tgaaaaaata cagattgtta cacaaatgct cgaattgggtg gaaaatcggg caagacaaat 420
 ggagttacac tcacagtgtt tccaagatcc tgctgaaagt gaacgagcct cagataaagc 480
 aaagatggat tccagccaac cagaaagatc ttcaagaaga ccccgaggc agcggaccag 540
 tgaaagccgt gatttatgtc acatggcaaa tgggattgaa gactgtgatg atcagccacc 600
 taaagaaaag aaatccaagt cagcaaagaa aaagaaacgc tccaaggcca agcaggaaag 660
 ggaagcttca cctgttgagt ttgcaataga tcctaatagaa cctacatact gcttatgcaa 720
 ccaagtgtct tatggggaga tgataggatg tgacaatgaa cagtgtccaa ttgaatgggt 780
 tcacttttca tgtgtttcac ttacctataa accaaagggg aaatgggtatt gcccaaagt 840
 caggggagat aatgagaaaa caatggacaa aagtactgaa aagacaaaaa aggatagaag 900
 atcgaggtag taaaggccat ccacatttta aagggttatt tgtcttttat ataattcgtt 960
 tgctttcaga aaatgtttta gggtaaagtc ataagactat gcaataattt ttaatcatta 1020
 gtattaatgg tgtattaaaa gttgtgtgac tttgaaaaaa aaaaaaaaaa aaaaaaaaaa 1080

<210> 3
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Degenerate
primer used to isolate p33ING2 nucleic acids

<400> 3
Met Leu Gly Gln Gln Gln Gln
1 5

<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Degenerate
primer used to isolate p33ING2 nucleic acid

<400> 4
Lys Lys Asp Arg Arg Ser Arg
1 5

<210> 5
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide 7-26
of p33ING2 (KMP1)

<400> 5
Gln Gln Leu Tyr Ser Ser Ala Ala Leu Leu Thr Gly Glu Arg Ser Arg
1 5 10 15

Leu Leu Thr Cys
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<210> 6
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: missense
p33ING2 sequence - Arg 153 to Ser

<400> 6
Met Leu Gly Gln Gln Gln Gln Gln Leu Tyr Ser Ser Ala Ala Leu Leu
1 5 10 15

Thr Gly Glu Arg Ser Arg Leu Leu Thr Cys Tyr Val Gln Asp Tyr Leu
20 25 30

Glu	Cys	Val	Glu	Ser	Leu	Pro	His	Asp	Met	Gln	Arg	Asn	Val	Ser	Val	35	40	45
Leu	Arg	Glu	Leu	Asp	Asn	Lys	Tyr	Gln	Glu	Thr	Leu	Lys	Glu	Ile	Asp	50	55	60
Asp	Val	Tyr	Glu	Lys	Tyr	Lys	Lys	Glu	Asp	Asp	Leu	Asn	Gln	Lys	Lys	65	70	75
Arg	Leu	Gln	Gln	Leu	Leu	Gln	Arg	Ala	Leu	Ile	Asn	Ser	Gln	Glu	Leu	85	90	95
Gly	Asp	Glu	Lys	Ile	Gln	Ile	Val	Thr	Gln	Met	Leu	Glu	Leu	Val	Glu	100	105	110
Asn	Arg	Ala	Arg	Gln	Met	Glu	Leu	His	Ser	Gln	Cys	Phe	Gln	Asp	Pro	115	120	125
Ala	Glu	Ser	Glu	Arg	Ala	Ser	Asp	Lys	Ala	Lys	Met	Asp	Ser	Ser	Gln	130	135	140
Pro	Glu	Arg	Ser	Ser	Arg	Arg	Pro	Ser	Arg	Gln	Arg	Thr	Ser	Glu	Ser	145	150	155
Arg	Asp	Leu	Cys	His	Met	Ala	Asn	Gly	Ile	Glu	Asp	Cys	Asp	Asp	Gln	165	170	175
Pro	Pro	Lys	Glu	Lys	Lys	Ser	Lys	Ser	Ala	Lys	Lys	Lys	Lys	Arg	Ser	180	185	190
Lys	Ala	Lys	Gln	Glu	Arg	Glu	Ala	Ser	Pro	Val	Glu	Phe	Ala	Ile	Asp	195	200	205
Pro	Asn	Glu	Pro	Thr	Tyr	Cys	Leu	Cys	Asn	Gln	Val	Ser	Tyr	Gly	Glu	210	215	220
Met	Ile	Gly	Cys	Asp	Asn	Glu	Gln	Cys	Pro	Ile	Glu	Trp	Phe	His	Phe	225	230	235
Ser	Cys	Val	Ser	Leu	Thr	Tyr	Lys	Pro	Lys	Gly	Lys	Trp	Tyr	Cys	Pro	245	250	255
Lys	Cys	Arg	Gly	Asp	Asn	Glu	Lys	Thr	Met	Asp	Lys	Ser	Thr	Glu	Lys	260	265	270
Thr	Lys	Lys	Asp	Arg	Arg	Ser	Arg									275	280	

<210> 7
 <211> 423
 <212> DNA
 <213> Homo sapiens

<220>
 <223> p 33ING2 genomic DNA sequence (exon 1/intron)
 GenBank Accession No. HSING2S1

<221> exon
 <222> (1)..(239)
 <221> intron
 <222> (240)..(>423)

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 ggagcggagc cggctgctca cctgctacgt gcaggactac cttgagtgcg tggagtcgct 180
 gccccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaagg 240
 tagggggcgc ggggctgccg gcctcgggag ccggtggcgg ggagcctgtc cgggggagtg 300
 ccaccttccc tttctcccggt gacagtctcc ccgagcgcac cgagggtctg ccgagcggga 360
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 aga 423

<210> 8
 <211> 279
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: p33ING1

<400> 8
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 20 25 30
 Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
 35 40 45
 Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
 50 55 60
 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
 65 70 75 80
 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
 85 90 95
 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
 100 105 110
 Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Ala Gly Asn Ser Gly Lys
 115 120 125
 Ala Gly Ala Asp Arg Pro Lys Gly Glu Ala Ala Ala Gln Ala Asp Lys
 130 135 140

Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
 145 150 155 160
 Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro
 165 170 175
 Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala
 180 185 190
 Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
 195 200 205
 Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
 210 215 220
 Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
 225 230 235 240
 Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
 245 250 255
 Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
 260 265 270
 Lys Glu Arg Ala Tyr Asn Arg
 275

<210> 9
 <211> 279
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide 1-17
 and C of p33ING1 (KMP2)

<400> 9
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 Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
 35 40 45
 Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
 50 55 60
 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
 65 70 75 80
 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
 85 90 95
 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
 100 105 110

Phe	Glu	Ala	Gln	Gln	Glu	Leu	Gly	Asp	Thr	Ala	Gly	Asn	Ser	Gly	Lys	115	120	125
Ala	Gly	Ala	Asp	Arg	Pro	Lys	Gly	Glu	Ala	Ala	Ala	Gln	Ala	Asp	Lys	130	135	140
Pro	Asn	Ser	Lys	Arg	Ser	Arg	Arg	Gln	Arg	Asn	Asn	Glu	Asn	Arg	Glu	145	150	155
Asn	Ala	Ser	Ser	Asn	His	Asp	His	Asp	Asp	Gly	Ala	Ser	Gly	Thr	Pro	165	170	175
Lys	Glu	Lys	Lys	Ala	Lys	Thr	Ser	Lys	Lys	Lys	Lys	Arg	Ser	Lys	Ala	180	185	190
Lys	Ala	Glu	Arg	Glu	Ala	Ser	Pro	Ala	Asp	Leu	Pro	Ile	Asp	Pro	Asn	195	200	205
Glu	Pro	Thr	Tyr	Cys	Leu	Cys	Asn	Gln	Val	Ser	Tyr	Gly	Glu	Met	Ile	210	215	220
Gly	Cys	Asp	Asn	Asp	Glu	Cys	Pro	Ile	Glu	Trp	Phe	His	Phe	Ser	Cys	225	230	235
Val	Gly	Leu	Asn	His	Lys	Pro	Lys	Gly	Lys	Trp	Tyr	Cys	Pro	Lys	Cys	245	250	255
Arg	Gly	Glu	Asn	Glu	Lys	Thr	Met	Asp	Lys	Ala	Leu	Glu	Lys	Ser	Lys	260	265	270
Lys	Glu	Arg	Ala	Tyr	Asn	Arg										275		

<210> 10
<211> 974
<212> DNA
<213> Homo sapiens

<220>

<223> p33ING2 genomic DNA sequence (Exon 2/intron)
GenBank Accession No. HSING2S2

<221> intron

<222> (<1>)..(123)

<221> exon

<222> (124)..(938)

<400> 10

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tagaaacgtt aaaggaaatt gatgatgtct acgaaaaata taagaaagaa gatgatttaa 180
accagaagaa acgtctacag cagcttctcc agagagcact aattaatagt caagaattgg 240
gagatgaaaa aatacagatt gttacacaaa tgctcgaatt ggtggaaaat cgggcaagac 300
aaatggagtt acactcacag tgtttccaag atcctgctga aagtgaacga gcctcagata 360
aagcaaagat ggattccagc caaccagaaa gatcttcaag aagaccccg caggcagcga 420
ccagtgaag ccgtgattta tgtcacatgg caaatgggat tgaagactgt gatgatcagc 480
cacctaaaga aaagaaatcc aagtcagcaa agaaaaagaa acgctccaag gccaagcagg 540
aaaggaagc ttcacctgtt gagtttgcaa tagatcctaa tgaacctaca tactgcttat 600
gcaaccaagt gtcttatggg gagatgatag gatgtgacaa tgaacagtgt ccaattgaat 660
ggtttcactt ttcatgtgtt tcacttacct ataaaccaa ggggaaatgg tattgcccaa 720
agtgcagggg agataatgag aaaacaatgg acaaaagtac tgaaaagaca aaaaaggata 780
gaagatcgag gtagtaaagg ccatccacat tttaaagggt tatttgctt ttatataatt 840
cgtttgctt cagaaaatgt tttagggtaa atgcataaga ctatgcaata atttttaatc 900
attagtatta atggtgtatt aaaagttgtt gtactttgtc tgtgacctta attttctgca 960
ctgagttacc aaat                                     974
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